

SEQUENCE LISTING

(1) GENERAL INFORMATION

5 (i) APPLICANT: University of Utrecht, Technology Foundation

(ii) TITLE OF THE INVENTION: Vaccine

(iii) NUMBER OF SEQUENCES: 10

10 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SmithKline Beecham, Corporate IP Department
(B) STREET: Two, New Horizons Court,
(C) CITY: Brentford
15 (D) STATE: Middlesex
(E) COUNTRY: United Kingdom
(F) ZIP: TW8 9EP

(v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

25 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: DALTON, Marcus Jonathan William
(B) REGISTRATION NUMBER: XXXXXX
(C) REFERENCE/DOCKET NUMBER: B45106

(ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (0181) 975 6348
(B) TELEFAX: (0181) 975 6177

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain BNCV

(ix) FEATURE:

15 (A) NAME/KEY: Coding Sequence

(B) LOCATION: 100...2274

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.1:

20

TCTTGATTT TGTAAATTCA CTATAAAAAC GGGTTGATAT TATCTGTACA TATTAATATA 60
 ATGATAATTA TTATTAATCA AATAGGAGGA AAAGTAGGG ATG TGT AAA CCG AAT 114
Met Cys Lys Pro Asn
1 5

25

TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG GCA TCT TGT ATC GGC 162
 Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu Ala Ser Cys Ile Gly
 10 15 20

30 GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA ACG CCG ACC GCG TAC 210
Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser Thr Pro Thr Ala Tyr
25 30 35

35 CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT CCG CCC CCT GCC AAA 258
Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr Pro Pro Pro Ala Lys
40 45 50

CCT TCT ATA GAA ATC ACG CCG GTC AAC CGG CCC GCC GTC GGT GCG GCA	306
Pro Ser Ile Glu Ile Thr Pro Val Asn Arg Pro Ala Val Gly Ala Ala	

3

	ATG CGG CTG CCA AGG CGG AAT ACT GCT TTT CAT CGT GAA GAT GGC ACG	354
	Met Arg Leu Pro Arg Arg Asn Thr Ala Phe His Arg Glu Asp Gly Thr	
70	75	80
		85
5	GAA ATT CCA AAT AGC AAA CAA GCA GAA AAG CTG TCG TTT CAA GAA	402
	Glu Ile Pro Asn Ser Lys Gln Ala Glu Glu Lys Leu Ser Phe Gln Glu	
	90	95
		100
10	GGT GAT GTT CTG TTT TTA TAC GGT TCA AAA GGA AAT AAA CTT CAA CAA	450
	Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly Asn Lys Leu Gln Gln	
	105	110
		115
15	CTT AAA AGC GAA ATT CAT AAA CGT GAT TCC GAT GTA GAA ATT AGG ACA	498
	Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp Val Glu Ile Arg Thr	
	120	125
		130
	TCA GAA AAG GAA AAT AAA AAA TAT GAT TAT AAA TTT GTA GAT GCA GGT	546
	Ser Glu Lys Glu Asn Lys Lys Tyr Asp Tyr Lys Phe Val Asp Ala Gly	
	135	140
		145
20	TAT GTA TAT GTA AAG GGA AAA GAT GAA ATT AAG TGG ACT TCA GAT TAC	594
	Tyr Val Tyr Val Lys Gly Lys Asp Glu Ile Lys Trp Thr Ser Asp Tyr	
	150	155
		160
		165
25	AAG CAG TTT TCC AAC CGC TTA GGT TAT GAC GGT TTT GTA TAT TAT TCC	642
	Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp Gly Phe Val Tyr Tyr Ser	
	170	175
		180
30	GGA GAA CGT CCT TCC CAA TCT TTA CCG AGT GCG GGA ACG GTG GAA TAT	690
	Gly Glu Arg Pro Ser Gln Ser Leu Pro Ser Ala Gly Thr Val Glu Tyr	
	185	190
		195
35	TCT GGT AAC TGG CAA TAT ATG ACC GAT GCC AAA CGT CAT CGA GCA GGT	738
	Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala Lys Arg His Arg Ala Gly	
	200	205
		210
	AAG GCG GTT GGC ATT GAC AAT TTG GGT TAT TAC ACA TTT TAT GGT AAC	786
	Lys Ala Val Gly Ile Asp Asn Leu Gly Tyr Tyr Thr Phe Tyr Gly Asn	
	215	220
		225
40	GAT GTT GGT GCA ACT TCT TAT GCG GCT AAG GAT GTC GAC GAA AGG GAA	834
	Asp Val Gly Ala Thr Ser Tyr Ala Ala Lys Asp Val Asp Glu Arg Glu	
	230	235
		240
		245

	AAA CAT CCT GCT AAA TAT ACG GTA GAT TTC GGT AAC AAA ACC CTG ACG	882		
5	Lys His Pro Ala Lys Tyr Thr Val Asp Phe Gly Asn Lys Thr Leu Thr			
	250	255	260	
	GGC GAG CTG ATT AAA AAC CAA TAT GTC AAA CCC AGT GAG AAG CAA AAA	930		
	Gly Glu Leu Ile Lys Asn Gln Tyr Val Lys Pro Ser Glu Lys Gln Lys			
	265	270	275	
10	CCG CTG ACC ATT TAC AAC ATC ACT GCC GAT TTA AAC GGC AAC CGC TTT	978		
	Pro Leu Thr Ile Tyr Asn Ile Thr Ala Asp Leu Asn Gly Asn Arg Phe			
	280	285	290	
15	ACC GGC AGT GCC AAG GTC AAT CCT GAT TTA GCG AAA AGC CAT GCC AAT	1026		
	Thr Gly Ser Ala Lys Val Asn Pro Asp Leu Ala Lys Ser His Ala Asn			
	295	300	305	
20	AAG GAG CAT TTG TTT TTC CAT GCC GAT GCC GAT CAG CGG CTT GAG GGC	1074		
	Lys Glu His Leu Phe Phe His Ala Asp Ala Asp Gln Arg Leu Glu Gly			
	310	315	320	325
	GGT TTT TTC GGC GAT AAG GGG GAA GAG CTT GCC GGA CGG TTT ATC AGC	1122		
	Gly Phe Phe Gly Asp Lys Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser			
	330	335	340	
25	AAC GAC AAC AGC GTA TTC GGT GTA TTC GCA GGC AAA CAA AAT AGC CCC	1170		
	Asn Asp Asn Ser Val Phe Gly Val Phe Ala Gly Lys Gln Asn Ser Pro			
	345	350	355	
30	GTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT TCT CTG AAA ATT TCC	1218		
	Val Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile Ser			
	360	365	370	
35	GTT GAT GAG GCA AGT GGT GAA AAT CCC CGA CCG TTT GCC ATT TCT CCT	1266		
	Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Ala Ile Ser Pro			
	375	380	385	
	ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT GTC GAA GGG CAT GAA	1314		
	Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly His Glu			
40	390	395	400	405

5

ATT CCT TTG GTT AGC CAA GAG AAA ACC ATC GAG CTT GCC GAC GGC AGG . 1362		
Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly Arg		
410	415	420
5 AAA ATG ACC GTC AGT GCT TGT TGC GAC TTT TTG ACC TAT GTG AAA CTC 1410		
Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys Leu		
425	430	435
10 GGA CGG ATA AAA ACC GAA CGC CCC GCC GCC AAA CCG AAG GCG CAG GAC 1458		
Gly Arg Ile Lys Thr Glu Arg Pro Ala Ala Lys Pro Lys Ala Gln Asp		
440	445	450
15 GAA GAG GAT TCG GAC ATT GAT AAT GGC GAA GAA AGC GAA GAC GAA ATC 1506		
Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu Ile		
455	460	465
20 GGC GAT GAA GAA GAA GGC ACC GAA GAT GCA GCC GCA GGA GAT GAA GGC 1554		
Gly Asp Glu Glu Gly Thr Glu Asp Ala Ala Gly Asp Glu Gly		
470	475	480
25 485		
AGC GAA GAA GAC GAA GCC ACA GAA AAC GAA GAC GGC GAA GAA GAC GAA 1602		
Ser Glu Glu Asp Glu Ala Thr Glu Asn Glu Asp Gly Glu Glu Asp Glu		
490	495	500
30 505	510	515
AAC GCC ATC CTG CCT GTC CCG GAA GCC TCT AAA GGC AGG GAT ATC GAC 1650		
Asn Ala Ile Leu Pro Val Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp		
520	525	530
35 535	540	545
CTT TTC CTG AAA GGT ATC CGC ACG GCA GAA ACG AAT ATT CCG CAA ACT 1746		
Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asn Ile Pro Gln Thr		
550	555	560
40 565		
GGA GAA GCA CGC TAT ACC GGC ACT TGG GAA GCG CGT ATC GGC AAA CCC 1794		
Gly Glu Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro		
570	575	580
ATT CAA TGG GAC AAT CAT GCG GAT AAA GAA GCG GCA AAA GCA GTA TTT 1842		
Ile Gln Trp Asp Asn His Ala Asp Lys Glu Ala Ala Lys Ala Val Phe		

	ACC GTT GAT TTC GGC AAG AAA TCG ATT TCC GGA ACG CTG ACG GAG AAA	1890
	Thr Val Asp Phe Gly Lys Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys	
	585	590
5		595
	AAC GGT GTA GAA CCT GCT TTC CGT ATT GAA AAC GGC GTG ATT GAG GGC	1938
	Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn Gly Val Ile Glu Gly	
	600	605
	610	
10	AAC GGT TTC CAT GCG ACA GCG CGC ACT CGG GAT GAC GGC ATC GAC CTT	1986
	Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp Asp Gly Ile Asp Leu	
	615	620
	625	
15	TCC GGG CAG GGT TCG ACC AAA CCG CAG ATC TTC AAA GCT AAT GAT CTT	2034
	Ser Gly Gln Gly Ser Thr Lys Pro Gln Ile Phe Lys Ala Asn Asp Leu	
	630	635
	640	645
20	CGT GTA GAA GGA GGA TTT TAC GGC CCG AAG GCG GAG GAA TTG GGC GGT	2082
	Arg Val Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly	
	650	655
	660	
	ATT ATT TTC AAT AAT GAT GGG AAA TCT CTT GGT ATA ACT GAA GGT ACT	2130
	Ile Ile Phe Asn Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Gly Thr	
	665	670
	675	
25	GAA AAT AAA GTT GAA GCT GAT GTT GAT GTT GAT GTT GAT GTT GAT GTT	2178
	Glu Asn Lys Val Glu Ala Asp Val Asp Val Asp Val Asp Val Asp Val	
	680	685
	690	
30	GAT GCT GAT GCT GAT GTT GAA CAG TTA AAA CCT GAA GTT AAA CCC CAA	2226
	Asp Ala Asp Ala Asp Val Glu Gln Leu Lys Pro Glu Val Lys Pro Gln	
	695	700
	705	
35	TTC GGC GTG GTA TTC GGT GCG AAG AAA GAT AAT AAA GAG GTG GAA AAA T	2275
	Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn Lys Glu Val Glu Lys	
	710	715
	720	725
	GA	2277

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 725 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: Neisseria meningitidis strain BNCV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
1 5 10 15

Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
20 25 30

20 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
35 40 45

Pro Pro Pro Ala Lys Pro Ser Ile Glu Ile Thr Pro Val Asn Arg Pro
50 55 60

Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn Thr Ala Phe His
25 65 70 75 80

Arg Glu Asp Gly Thr Glu Ile Pro Asn Ser Lys Gln Ala Glu Glu Lys
85 90 95

Leu Ser Phe Gln Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly
100 105 110

30 Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp
115 120 125

Val Glu Ile Arg Thr Ser Glu Lys Glu Asn Lys Lys Tyr Asp Tyr Lys
130 135 140

Phe Val Asp Ala Gly Tyr Val Tyr Val Lys Gly Lys Asp Glu Ile Lys
35 145 150 155 160

Trp Thr Ser Asp Tyr Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp Gly
165 170 175

Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln Ser Leu Pro Ser Ala
180 185 190
Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala Lys
195 200 205
5 Arg His Arg Ala Gly Lys Ala Val Gly Ile Asp Asn Leu Gly Tyr Tyr
210 215 220
Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser Tyr Ala Ala Lys Asp
225 230 235 240
Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr Thr Val Asp Phe Gly
10 245 250 255
Asn Lys Thr Leu Thr Gly Glu Leu Ile Lys Asn Gln Tyr Val Lys Pro
260 265 270
Ser Glu Lys Gln Lys Pro Leu Thr Ile Tyr Asn Ile Thr Ala Asp Leu
275 280 285
15 Asn Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Pro Asp Leu Ala
290 295 300
Lys Ser His Ala Asn Lys Glu His Leu Phe Phe His Ala Asp Ala Asp
305 310 315 320
Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu Glu Leu Ala
20 325 330 335
Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe Ala Gly
340 345 350
Lys Gln Asn Ser Pro Val Pro Ser Gly Lys His Thr Lys Ile Leu Asp
355 360 365
25 Ser Leu Lys Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro
370 375 380
Phe Ala Ile Ser Pro Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu
385 390 395 400
Val Glu Gly His Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu
30 405 410 415
Leu Ala Asp Gly Arg Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu
420 425 430
Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Ala Lys
435 440 445
35 Pro Lys Ala Gln Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu
450 455 460

Ser Glu Asp Glu Ile Gly Asp Glu Glu Glu Gly Thr Glu Asp Ala Ala
465 470 475 480

Ala Gly Asp Glu Gly Ser Glu Glu Asp Glu Ala Thr Glu Asn Glu Asp
485 490 495

5 Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Ser Ser Ala Glu
500 505 510

Gly Asn Gly Ser Ser Asn Ala Ile Leu Pro Val Pro Glu Ala Ser Lys
515 520 525

Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr
10 530 535 540

Asn Ile Pro Gln Thr Gly Glu Ala Arg Tyr Thr Gly Thr Trp Glu Ala
545 550 555 560

Arg Ile Gly Lys Pro Ile Gln Trp Asp Asn His Ala Asp Lys Glu Ala
565 570 575

15 Ala Lys Ala Val Phe Thr Val Asp Phe Gly Lys Lys Ser Ile Ser Gly
580 585 590

Thr Leu Thr Glu Lys Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn
595 600 605

Gly Val Ile Glu Gly Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp
20 610 615 620

Asp Gly Ile Asp Leu Ser Gly Gln Gly Ser Thr Lys Pro Gln Ile Phe
625 630 635 640

Lys Ala Asn Asp Leu Arg Val Glu Gly Gly Phe Tyr Gly Pro Lys Ala
645 650 655

25 Glu Glu Leu Gly Gly Ile Ile Phe Asn Asn Asp Gly Lys Ser Leu Gly
660 665 670

Ile Thr Glu Gly Thr Glu Asn Lys Val Glu Ala Asp Val Asp Val Asp
675 680 685

Val Asp Val Asp Val Asp Ala Asp Ala Asp Val Glu Gln Leu Lys Pro
30 690 695 700

Glu Val Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn
705 710 715 720

Lys Glu Val Glu Lys
725

10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- 10 (vi) ORIGINAL SOURCE:
(B) STRAIN: Neisseria meningitidis strain M981

(ix) FEATURE:

15 (A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2166

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20	ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG	48
	Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu	
	1 5 10 15	
25	GCA TCT TGC ATC GGC GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA	96
	Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser	
	20 25 30	
30	ACG CCG ACC GCG TAC CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT	144
	Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr	
	35 40 45	
35	TCG CCC CCT GCC GGG TCT TCG GTA GAA ACC ACG CCG GTC AAC CAG CCC	192
	Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Gln Pro	
	50 55 60	
40	GCC GTC GGT GCG GCA ATG CGG CTG TTG AGA CGG AAT ACT GCT TTT CAT	240
	Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Thr Ala Phe His	
	65 70 75 80	
40	CGT GAA GAT GGC ACG GCA ATT CCC GAT AGC AAA CAA GCA GAA GAA AAG	288
	Arg Glu Asp Gly Thr Ala Ile Pro Asp Ser Lys Gln Ala Glu Glu Lys	
	85 90 95	

11

CTG TCG TTT AAA GAA GGT GAT GTT CTG TTT TTA TAC GGT TCA AAA GAA 336
 Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Glu
 100 105 110

5 AAT AAA CTT CAA CAA CTT AAA AGC GAA ATT CAT AAA CGT AAT CCT GAG 384
 Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asn Pro Glu
 115 120 125

10 GCA AGC ATT ACC ACA TCG GAA AAT GAA AAT AAA AAA TAT AAT TAT CGG 432
 Ala Ser Ile Thr Thr Ser Glu Asn Glu Asn Lys Lys Tyr Asn Tyr Arg
 130 135 140

15 TTT GTC AGT GCC GGT TAT GTG TTT ACT AAA AAC GGA AAA GAT GAA ATT 480
 Phe Val Ser Ala Gly Tyr Val Phe Thr Lys Asn Gly Lys Asp Glu Ile
 145 150 155 160

20 GAG AAA ACA TCG GAT GAA AAG CAG TTT TCT AAT CGT TTA GGC TAT GAC 528
 Glu Lys Thr Ser Asp Glu Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp
 165 170 175

GGT TTT GTA TAT TAT CTC GGA GAA CAT CCT TCC CAA TCT TTA CCG AGC 576
 Gly Phe Val Tyr Tyr Leu Gly Glu His Pro Ser Gln Ser Leu Pro Ser
 180 185 190

25 GCG GGA ACG GTG AAA TAT TCC GGC AAC TGG CAA TAT ATG ACC GAT GCC 624
 Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala
 195 200 205

30 ATA CGT CAT CGG AGA GGT AAG GGG GTT TCC AGT GTG GAT TTG GGT TAT 672
 Ile Arg His Arg Arg Gly Lys Gly Val Ser Ser Val Asp Leu Gly Tyr
 210 215 220

35 ACC ACA TAT TAT GGT AAT GAA ATT GGG GCA GCT TCT TAT GAG GCT AGG 720
 Thr Thr Tyr Tyr Gly Asn Glu Ile Gly Ala Ala Ser Tyr Glu Ala Arg
 225 230 235 240

40 GAT GCC GAT GGC CGG GAA AAA CAT CCT GCC GAA TAT ACG GTT AAT TTC 768
 Asp Ala Asp Gly Arg Glu Lys His Pro Ala Glu Tyr Thr Val Asn Phe
 245 250 255

GAC AAA AAA AAC CTG GAA GGT AAG TTG ATT AAA AAT CAG TAT GTG CAA 816
 Asp Lys Lys Asn Leu Glu Gly Lys Leu Ile Lys Asn Gln Tyr Val Gln
 260 265 270

	AAG AGA GAT GAT CCT AAA AAT CCA CTG ACC ATT TAC AAC ATT ACC GCA	864		
	Lys Arg Asp Asp Pro Lys Asn Pro Leu Thr Ile Tyr Asn Ile Thr Ala			
5	275	280	285	
	ACA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC AAA GTT AGC ACC GAG	912		
	Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Ser Thr Glu			
	290	295	300	
10	GTG AAG ACG CAA CAC GCT GAT AAA GAA TAT TTG TTT TTC CAT ACC GAT	960		
	Val Lys Thr Gln His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr Asp			
	305	310	315	320
15	GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC GAT AAC GGA GAA GAG	1008		
	Ala Asp Gln Arg Leu Glu Gly Phe Phe Gly Asp Asn Gly Glu Glu			
	325	330	335	
20	CTT GCC GGG CGG TTT ATC AGT AAC GAC AAC AGC GTA TTC GGC GTG TTC	1056		
	Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe			
	340	345	350	
25	GCA GGC AAA CAA AAA ACA GAG ACA GCA AAC GCA TCA GAT ACA AAT CCT	1104		
	Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn Pro			
	355	360	365	
30	GCC CTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT TCT CTA AAA ATT	1152		
	Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile			
	370	375	380	
35	TCC GTT GAC GAG GCG ACT GAT GAC CAT GCC CGT AAG TTT GCC ATT TCC	1200		
	Ser Val Asp Glu Ala Thr Asp Asp His Ala Arg Lys Phe Ala Ile Ser			
	385	390	395	400
40	ACT ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT GTC GAA GGG CGT	1248		
	Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly Arg			
	405	410	415	
	GAA ATT CCT TTG GTT AGC CAA GAG AAA ACC ATC GAG CTT GCC GAC GGC	1296		
	Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly			
	420	425	430	

13

AGG AAA ATG ACC ATC CGT GCT TGT TGC GAT TTT CTG ACC TAT GTG AAA 1344
 Arg Lys Met Thr Ile Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys
 435 440 445

5 CTC GGA CGG ATA AAA ACC GAC CGC CCC GCC GTC AAA CCG AAG GCG CAG 1392
 Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Val Lys Pro Lys Ala Gln
 450 455 460

10 GAT GAA GAG GAT TCG GAC ATT GAT AAT GGC GAA GAA AGC GAA GAC GAA 1440
 Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu
 465 470 475 480

15 ATT TCC GAA GAT GAT AAC GGC GAA GAT GAA GTC ACC GAA GAA GAG GAA 1488
 Ile Ser Glu Asp Asp Asn Gly Glu Asp Glu Val Thr Glu Glu Glu Glu
 485 490 495

20 GCT GAA GAA ACC GAA GAA GAA ACT GAT GAA GAC GAA GAG GAA GAA CCC 1536
 Ala Glu Glu Thr Glu Glu Thr Asp Glu Asp Glu Glu Glu Pro
 500 505 510

GAA GAA ACT GAA 1584
 Glu Glu Thr Glu
 515 520 525

25 GAA ACT GAA GAA AAA TCG CCG ACA GAA GAA GGC AAC GGC GGT TCA GGC 1632
 Glu Thr Glu Glu Lys Ser Pro Thr Glu Glu Gly Asn Gly Ser Gly
 530 535 540

30 AGC ATC CTG CCC ACT CCG GAA GCC TCT AAA GGC AGG GAC ATC GAC CTT 1680
 Ser Ile Leu Pro Thr Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu
 545 550 555 560

35 TTC CTG AAA GGT ATC CGC ACG GCG GAA GCC GAC ATT CCG CAA ATT GGA 1728
 Phe Leu Lys Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Ile Gly
 565 570 575

40 AAA GCA CGC TAT ACC GGC ACT TGG GAA GCG CGT ATC GGC GTG CCG GAT 1776
 Lys Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Val Pro Asp
 580 585 590

AAG AAA GGC GAA CAG CTA GAT GGC ACT ACG TCC ATT CAA AAG GAT AGC 1824
 Lys Lys Gly Glu Gln Leu Asp Gly Thr Thr Ser Ile Gln Lys Asp Ser
 595 600 605

TAT GCG AAT CAA GCG GCA AAA GCA GAA TTT GAC GTT GAT TTT GGT GCG	1872		
Tyr Ala Asn Gln Ala Ala Lys Ala Glu Phe Asp Val Asp Phe Gly Ala			
610	615	620	
AAG TCG CTT TCA GGT AAG TTG ACA GAA AAA AAT GAT ACA CAC CCC GCT	1920		
Lys Ser Leu Ser Gly Lys Leu Thr Glu Lys Asn Asp Thr His Pro Ala			
625	630	635	640
TTT TAT ATT GAA AAA GGT GTG ATT GAT GGC AAC GGT TTC CAC GCT TTG	1968		
Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala Leu			
645	650	655	
GCG CGT ACT CGT GAA AAT GGT GTT GAT TTG TCT GGG CAA GGT TCG ACT	2016		
Ala Arg Thr Arg Glu Asn Gly Val Asp Leu Ser Gly Gln Gly Ser Thr			
660	665	670	
AAT CCC CAA AGT TTT AAA GCC AGT AAT CTT CTC GTA GAA GGA GGA TTT	2064		
Asn Pro Gln Ser Phe Lys Ala Ser Asn Leu Leu Val Glu Gly Gly Phe			
675	680	685	
TAT GGT CCG CAG GCG GCA GAG TTG GGT GGT AAT ATT ATC GAC AGT GAC	2112		
Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser Asp			
690	695	700	
CGG AAA ATC GGC GTG GTA TTC GGT GCG AAG AAA GAT ATG CAG GAG GTG	2160		
Arg Lys Ile Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val			
705	710	715	720
GAA AAA TGA	2169		
Glu Lys			

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 amino acids

5 (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: Neisseria meningitidis strain M981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu			
1	5	10	15
Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser			
20	25	30	
Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr			
35	40	45	
Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Gln Pro			
50	55	60	
Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Thr Ala Phe His			
65	70	75	80
Arg Glu Asp Gly Thr Ala Ile Pro Asp Ser Lys Gln Ala Glu Glu Lys			
85	90	95	
Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Glu			
100	105	110	
Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asn Pro Glu			
115	120	125	
Ala Ser Ile Thr Thr Ser Glu Asn Glu Asn Lys Lys Tyr Asn Tyr Arg			
130	135	140	
Phe Val Ser Ala Gly Tyr Val Phe Thr Lys Asn Gly Lys Asp Glu Ile			
145	150	155	160
Glu Lys Thr Ser Asp Glu Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp			
165	170	175	
Gly Phe Val Tyr Tyr Leu Gly Glu His Pro Ser Gln Ser Leu Pro Ser			
180	185	190	
40 Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala			
195	200	205	
Ile Arg His Arg Arg Gly Lys Gly Val Ser Ser Val Asp Leu Gly Tyr			
210	215	220	

Thr Thr Tyr Tyr Gly Asn Glu Ile Gly Ala Ala Ser Tyr Glu Ala Arg
225 230 235 240
Asp Ala Asp Gly Arg Glu Lys His Pro Ala Glu Tyr Thr Val Asn Phe
245 250 255
5 Asp Lys Lys Asn Leu Glu Gly Lys Leu Ile Lys Asn Gln Tyr Val Gln
260 265 270
Lys Arg Asp Asp Pro Lys Asn Pro Leu Thr Ile Tyr Asn Ile Thr Ala
275 280 285
Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Ser Thr Glu
10 290 295 300
Val Lys Thr Gln His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr Asp
305 310 315 320
Ala Asp Gln Arg Leu Glu Gly Phe Phe Gly Asp Asn Gly Glu Glu
325 330 335
15 Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe
340 345 350
Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn Pro
355 360 365
Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile
20 370 375 380
Ser Val Asp Glu Ala Thr Asp Asp His Ala Arg Lys Phe Ala Ile Ser
385 390 395 400
Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly Arg
405 410 415
25 Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly
420 425 430
Arg Lys Met Thr Ile Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys
435 440 445
Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Val Lys Pro Lys Ala Gln
30 450 455 460
Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu
465 470 475 480
Ile Ser Glu Asp Asp Asn Gly Glu Asp Glu Val Thr Glu Glu Glu Glu
485 490 495
35 Ala Glu Glu Thr Glu Glu Glu Thr Asp Glu Asp Glu Glu Glu Pro
500 505 510
Glu Glu Thr Glu
515 520 525
Glu Thr Glu Glu Lys Ser Pro Thr Glu Glu Gly Asn Gly Gly Ser Gly
40 530 535 540
Ser Ile Leu Pro Thr Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu
545 550 555 560

17

Phe Leu Lys Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Ile Gly
565 570 575
Lys Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Val Pro Asp
580 585 590
5 Lys Lys Gly Glu Gln Leu Asp Gly Thr Thr Ser Ile Gln Lys Asp Ser
595 600 605
Tyr Ala Asn Gln Ala Ala Lys Ala Glu Phe Asp Val Asp Phe Gly Ala
610 615 620
Lys Ser Leu Ser Gly Lys Leu Thr Glu Lys Asn Asp Thr His Pro Ala
10 625 630 635 640
Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala Leu
645 650 655
Ala Arg Thr Arg Glu Asn Gly Val Asp Leu Ser Gly Gln Gly Ser Thr
660 665 670
15 Asn Pro Gln Ser Phe Lys Ala Ser Asn Leu Leu Val Glu Gly Phe
675 680 685
Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser Asp
690 695 700
Arg Lys Ile Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val
20 705 710 715 720
Glu Lys

18

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- 10 (vi) ORIGINAL SOURCE:
 (B) STRAIN: *Neisseria meningitidis* strain H44/76

(ix) FEATURE:

- 15 (A) NAME/KEY: Coding Sequence

- (B) LOCATION: 1...2223

- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

20	ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG	48
	Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu	
	1 5 10 15	
25	GCA TCT TGT ATT GGC GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA	96
	Ala Ser Cys Ile Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser	
	20 25 30	
30	ACG CCG ACC GCG TAC CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT	144
	Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr	
	35 40 45	
35	CCG CCC CCT GCC AAA CCT TCT ATA GAA ACC ACG CCG GTG CCG TCA ACC	192
	Pro Pro Pro Ala Lys Pro Ser Ile Glu Thr Thr Pro Val Pro Ser Thr	
	50 55 60	
40	GGG CCT GCC GTC GGT GCG GCA ATG CGG CTG TTG AGG CGG ATT TTC GCA	240
	Gly Pro Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Ile Phe Ala	
	65 70 75 80	
45	ACT TCT GAT AAG GTT GGC AAT GAT TTT CCA AAT AGC AAA CAA GCA GAA	288
	Thr Ser Asp Lys Val Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu	
	85 90 95	

	19		
5	GAA AAG CTG TCG TTT AAA GAA GGT GAT GTT CTG TTT TTA TAC GGT TCA Glu Lys Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser 100	105	110
10	AAA AAA GAT AAA CTT CAG TGG CTT AAG GAT AAA ATT CAT CAA CGC AAT Lys Lys Asp Lys Leu Gln Trp Leu Lys Asp Lys Ile His Gln Arg Asn 115	120	125
15	CCT AAT GTA GAA ATT AGG ACA TCA GAA AAT GAA AAT AAA AAA TAT GGT Pro Asn Val Glu Ile Arg Thr Ser Glu Asn Glu Asn Lys Lys Tyr Gly 130	135	140
20	TAT GAA TTT GTG GAT GCC GGT TAT GTA TAT ACT AAA AAC GGA ACA GAT Tyr Glu Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asn Gly Thr Asp 145	150	155
25	160	165	170
30	GAA ATT GAG TGG ACT TCA AAT CGC AAG CAG TTT TCT AAT CGT TTT GGC Glu Ile Glu Trp Thr Ser Asn Arg Lys Gln Phe Ser Asn Arg Phe Gly 175	180	185
35	190	195	200
40	205	210	215
45	220	225	230
50	235	240	245
55	250	255	260
60	265	270	275

TAT GTG CAA AAG AAA ACC GAT GAA AAG AAA CCA CTG ACC ATT TAC GAC		864	
Tyr Val Gln Lys Lys Thr Asp Glu Lys Lys Pro Leu Thr Ile Tyr Asp			
275	280	285	
5			
ATT ACC GCA ACA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC AAA GTT		912	
Ile Thr Ala Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val			
290	295	300	
10 AAC ACC GAG TTG AAG ACG AGC CAC GCT GAT AAA GAG CAT TTG TTT TTC		960	
Asn Thr Glu Leu Lys Thr Ser His Ala Asp Lys Glu His Leu Phe Phe			
305	310	315	320
15 CAT ACC GAT GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC GAT AAG		1008	
His Thr Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys			
325	330	335	
20 GGG GAA GAG CTT GCC GGA CGG TTT ATC AGC AAC GAC AAC AGC GTA TTC		1056	
Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe			
340	345	350	
25 GGC GTA TTC GCA GGC AAA AAA ACA AAC GCA TCA AAC GCA GCA GAT ACA		1104	
Gly Val Phe Ala Gly Lys Lys Thr Asn Ala Ser Asn Ala Ala Asp Thr			
355	360	365	
30 AAT CCT GCT ATG CCG TCT GAA AAA CAC ACC AAA ATC TTG GAT TCT CTG		1152	
Asn Pro Ala Met Pro Ser Glu Lys His Thr Lys Ile Leu Asp Ser Leu			
370	375	380	
35 AAA ATT TCC GTT GAC GAG GCG ACG GAT AAA AAT GCC CGC CCG TTT GCC		1200	
Lys Ile Ser Val Asp Glu Ala Thr Asp Lys Asn Ala Arg Pro Phe Ala			
385	390	395	400
35 ATT TCC CCT CTG CCC GAT TTT GGC CAT CCC GAC AAA CTC CTT GTC GAA		1248	
Ile Ser Pro Leu Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu			
405	410	415	
40 GGG CGT GAA ATT CCT TTG GTT AGC CAA GAG AAA ACC ATC GAG CTT GCC		1296	
Gly Arg Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala			
420	425	430	

	GAC GGC AGG AAA ATG ACC GTC CGT GCT TGT TGC GAT TTT CTG ACC TAT	1344		
	Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr			
	435	440	445	
5	GTG AAA CTC GGA CGG ATA AAA ACT GAC CGC CCA GCA AGT AAA CCA AAG	1392		
	Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys Pro Lys			
	450	455	460	
10	GCG GAA GAT AAA GGG AAG GAT GAA GAG GAT ACA GGC GTT GGT AAC GAC	1440		
	Ala Glu Asp Lys Gly Lys Asp Glu Glu Asp Thr Gly Val Gly Asn Asp			
	465	470	475	480
15	GAA GAA GGC ACG GAA GAT GAA GCC GCA GAA GGC AGC GAA GGA GGC GAA	1488		
	Glu Glu Gly Thr Glu Asp Glu Ala Ala Glu Gly Ser Glu Gly Gly Glu			
	485	490	495	
20	GAC GAA ATC GGC GAT GAA GGA GGA GGT GCG GAA GAC GAA GCC GCA GAA	1536		
	Asp Glu Ile Gly Asp Glu Gly Gly Ala Glu Asp Glu Ala Ala Glu			
	500	505	510	
25	AAC GAA GGC GGC GAA GAA GAC GAA GCT GAA GAA CCT GAA GAA CCC GAA	1584		
	Asn Glu Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Pro Glu			
	515	520	525	
30	GAA GAA TCG CCG GCA GAA GGC GGC GGT GGT GGT TCA GAC GGC ATC CTG	1632		
	Glu Glu Ser Pro Ala Glu Gly Gly Gly Ser Asp Gly Ile Leu			
	530	535	540	
35	CCC GCT CCG GAA GCT CCT AAA GGC AGG GAT ATC GAC CTT TTC CTG AAA	1680		
	Pro Ala Pro Glu Ala Pro Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys			
	545	550	555	560
40	GGT ATC CGC ACG GCG GAA GCC GAC ATT CCG CAA ACT GGA AAA GCA CGC	1728		
	Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Thr Gly Lys Ala Arg			
	565	570	575	
	TAT ACC GGC ACT TGG GAA GCG CGT ATC AGC AAA CCC ATT CAA TGG GAC	1776		
	Tyr Thr Gly Thr Trp Glu Ala Arg Ile Ser Lys Pro Ile Gln Trp Asp			
	580	585	590	
	AAT CAT GCG GAT AAA AAA GCG GCA AAA GCA GAA TTT GAC GTT GAT TTC	1824		
	Asn His Ala Asp Lys Lys Ala Ala Lys Ala Glu Phe Asp Val Asp Phe			
	595	600	605	

	GGC GAG AAA TCG ATT TCC GGA ACG CTG ACG GAG AAA AAC GGT GTA CAA	1872
	Gly Glu Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys Asn Gly Val Gln	
	610 615 620	
5	CCT GCT TTC CAT ATT GAA AAC GGC GTG ATT GAG GGC AAT GGT TTC CAC	1920
	Pro Ala Phe His Ile Glu Asn Gly Val Ile Glu Gly Asn Gly Phe His	
	625 630 635 640	
10	GCG ACA GCG CGC ACT CGG GAT AAC GGC ATC AAT CTT TCG GGA AAT GAT	1968
	Ala Thr Ala Arg Thr Arg Asp Asn Gly Ile Asn Leu Ser Gly Asn Asp	
	645 650 655	
15	TCG ACT AAT CCT CCA AGT TTC AAA GCC AAT AAT CTT CTT GTA ACA GGC	2016
	Ser Thr Asn Pro Pro Ser Phe Lys Ala Asn Asn Leu Leu Val Thr Gly	
	660 665 670	
20	GGC TTT TAC GGC CCG CAG GCG GAG GAA TTG GGC GGT ACT ATT TTC AAT	2064
	Gly Phe Tyr Gly Pro Gln Ala Glu Glu Leu Gly Thr Ile Phe Asn	
	675 680 685	
	AAT GAT GGG AAA TCT CTT GGT ATA ACT GAA GAT ACT GAA AAT GAA GCT	2112
	Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Asp Thr Glu Asn Glu Ala	
	690 695 700	
25	GAA GCT GAA GTT GAA AAT GAA GCT GGT GTT GGC GAA CAG TTA AAA CCT	2160
	Glu Ala Glu Val Glu Asn Glu Ala Gly Val Gly Glu Gln Leu Lys Pro	
	705 710 715 720	
30	GAA GCT AAA CCC CAA TTC GGC GTG GTA TTC GGT GCG AAG AAA GAT AAT	2208
	Glu Ala Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn	
	725 730 735	
	AAA GAG GTG GAA AAA TGA	2226
35	Lys Glu Val Glu Lys	
	740	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 741 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 10 (v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:
(B) STRAIN: Neisseria meningitidis strain H44/76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

15 Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu
1 5 10 15
Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
20 25 30
20 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
35 40 45
Pro Pro Pro Ala Lys Pro Ser Ile Glu Thr Thr Pro Val Pro Ser Thr
50 55 60
Gly Pro Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Ile Phe Ala
25 65 70 75 80
Thr Ser Asp Lys Val Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu
85 90 95
Glu Lys Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser
100 105 110
30 Lys Lys Asp Lys Leu Gln Trp Leu Lys Asp Lys Ile His Gln Arg Asn
115 120 125
Pro Asn Val Glu Ile Arg Thr Ser Glu Asn Glu Asn Lys Lys Tyr Gly
130 135 140
Tyr Glu Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asn Gly Thr Asp
35 145 150 155 160
Glu Ile Glu Trp Thr Ser Asn Arg Lys Gln Phe Ser Asn Arg Phe Gly
165 170 175
Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu
180 185 190
40 Pro Ser Ala Gly Thr Val Gln Tyr Ser Gly Asn Trp Gln Tyr Met Thr
195 200 205
Asp Ala Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp
210 215 220

24

Leu Gly Tyr Leu Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr
 225 230 235 240
 Ala Ala Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr
 245 250 255
 5 Val Asp Phe Asp Lys Lys Thr Leu Thr Gly Gln Leu Ile Lys Asn Gln
 260 265 270
 Tyr Val Gln Lys Lys Thr Asp Glu Lys Lys Pro Leu Thr Ile Tyr Asp
 275 280 285
 Ile Thr Ala Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val
 10 290 295 300
 Asn Thr Glu Leu Lys Thr Ser His Ala Asp Lys Glu His Leu Phe Phe
 305 310 315 320
 His Thr Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys
 325 330 335
 15 Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe
 340 345 350
 Gly Val Phe Ala Gly Lys Lys Thr Asn Ala Ser Asn Ala Ala Asp Thr
 355 360 365
 Asn Pro Ala Met Pro Ser Glu Lys His Thr Lys Ile Leu Asp Ser Leu
 20 370 375 380
 Lys Ile Ser Val Asp Glu Ala Thr Asp Lys Asn Ala Arg Pro Phe Ala
 385 390 395 400
 Ile Ser Pro Leu Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu
 405 410 415
 25 Gly Arg Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala
 420 425 430
 Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr
 435 440 445
 Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys Pro Lys
 30 450 455 460
 Ala Glu Asp Lys Gly Lys Asp Glu Glu Asp Thr Gly Val Gly Asn Asp
 465 470 475 480
 Glu Glu Gly Thr Glu Asp Glu Ala Ala Glu Gly Ser Glu Gly Glu
 485 490 495
 35 Asp Glu Ile Gly Asp Glu Gly Gly Ala Glu Asp Glu Ala Ala Glu
 500 505 510
 Asn Glu Gly Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Pro Glu
 515 520 525
 Glu Glu Ser Pro Ala Glu Gly Gly Gly Ser Asp Gly Ile Leu
 40 530 535 540
 Pro Ala Pro Glu Ala Pro Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys
 545 550 555 560

25

Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Thr Gly Lys Ala Arg
565 570 575
Tyr Thr Gly Thr Trp Glu Ala Arg Ile Ser Lys Pro Ile Gln Trp Asp
580 585 590
5 Asn His Ala Asp Lys Lys Ala Ala Lys Ala Glu Phe Asp Val Asp Phe
595 600 605
Gly Glu Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys Asn Gly Val Gln
610 615 620
Pro Ala Phe His Ile Glu Asn Gly Val Ile Glu Gly Asn Gly Phe His
10 625 630 635 640
Ala Thr Ala Arg Thr Arg Asp Asn Gly Ile Asn Leu Ser Gly Asn Asp
645 650 655
Ser Thr Asn Pro Pro Ser Phe Lys Ala Asn Asn Leu Leu Val Thr Gly
660 665 670
15 Gly Phe Tyr Gly Pro Gln Ala Glu Glu Leu Gly Thr Ile Phe Asn
675 680 685
Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Asp Thr Glu Asn Glu Ala
690 695 700
Glu Ala Glu Val Glu Asn Glu Ala Gly Val Gly Glu Gln Leu Lys Pro
20 705 710 715 720
Glu Ala Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn
725 730 735
Lys Glu Val Glu Lys
740

25

(2) INFORMATION FOR SEQ ID NO:7:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: cDNA
(vi) ORIGINAL SOURCE:
(B) STRAIN: Neisseria meningitidis strain M990
(ix) FEATURE:
40 (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...2259
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

	ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTA	48
5	Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu	
	1 5 10 15	
	GCA TCT TGT ATC GGC GGC AAT TTC GGC GTA CAG CCT GTT GTC GAA TCA	96
	Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser	
10	20 25 30	
	ACG CCG ACC GCG CCA ACT CTG TCA GAT TCC AAA TCT TCC AAT CCT GCG	144
	Thr Pro Thr Ala Pro Thr Leu Ser Asp Ser Lys Ser Ser Asn Pro Ala	
	35 40 45	
15		
	GAT AAG CCT GCT CCA GCT CCT GCC GAG CCT TCG GTA GAA ATC ACG CCG	192
	Asp Lys Pro Ala Pro Ala Glu Pro Ser Val Glu Ile Thr Pro	
	50 55 60	
20	GTC AAG CGG CCC GCC GTC GGT GCG GCA ATG CGG CTG CCA AGG CGG AAT	240
	Val Lys Arg Pro Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn	
	65 70 75 80	
25	ATC GCA ACT TTT GAT AAA AAT GGT AAT GAA ATT CCC AAT AGT AAG CAG	288
	Ile Ala Thr Phe Asp Lys Asn Gly Asn Glu Ile Pro Asn Ser Lys Gln	
	85 90 95	
30	GCA GAG GAG TAT CTG CCG CTC AAA GAG AAG GAT ATC CTG TTT TTA GAC	336
	Ala Glu Glu Tyr Leu Pro Leu Lys Glu Lys Asp Ile Leu Phe Leu Asp	
	100 105 110	
	GGT ACG CCG AAA GAA CAG GCT GAC AAA CTT AAA AAG GAA ATC AAC GGA	384
	Gly Thr Pro Lys Glu Gln Ala Asp Lys Leu Lys Lys Glu Ile Asn Gly	
	115 120 125	
35		
	CGG CAT CCT AAT GCA CCA ATC TAC ACG TCC GAT TTA AAA GAT GAT GCG	432
	Arg His Pro Asn Ala Pro Ile Tyr Thr Ser Asp Leu Lys Asp Asp Ala	
	130 135 140	
40	TAT CAA TAT AAA TAT GTC CGG GCC GGA TAT GTT TAT ACT AGA TAT GGA	480
	Tyr Gln Tyr Lys Tyr Val Arg Ala Gly Tyr Val Tyr Thr Arg Tyr Gly	
	145 150 155 160	

27

ACA GAT GAA ATC GAA CAG AAC TCA GGC GGT AAG CGG GTT ACC CAC CGC 528
 Thr Asp Glu Ile Glu Gln Asn Ser Gly Gly Lys Arg Val Thr His Arg
 165 170 175

5 TTA GGT TAT GAC GGT TTT GTA TAT TAT TCC GGA GAA CGT CCT TCC CAA 576
 Leu Gly Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln
 180 185 190

10 TCT TTA CCG AGT GCG GGA ACG GTG GAA TAT TCT GGT AAC TGG CAA TAT 624
 Ser Leu Pro Ser Ala Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr
 195 200 205

15 ATG ACC GAT GCC AAA CGT CAT CGA GCA GGT CAG GCG GTT GGC ATT GAC 672
 Met Thr Asp Ala Lys Arg His Arg Ala Gly Gln Ala Val Gly Ile Asp
 210 215 220

20 AAT TTG GGT TAT ATC ACA TTT TAT GGT AAC GAT GTT GGT GCA ACT TCT 720
 Asn Leu Gly Tyr Ile Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser
 225 230 235 240

25 TAT GCG GCT AAG GAT GTC GAC GAA AGG GAA AAG CAT CCT GCC AAA TAT 768
 Tyr Ala Ala Lys Asp Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr
 245 250 255

30 ACG GTT GAT TTT GAT AAC AAA ACC ATG AAT GGC AAG CTG ATT AAA AAT 816
 Thr Val Asp Phe Asp Asn Lys Thr Met Asn Gly Lys Leu Ile Lys Asn
 260 265 270

35 CAG TAT GTG CGA AAT AAA AAA GAT GAA CCC AAA AAA CCG CTG ACC ATT 864
 Gln Tyr Val Arg Asn Lys Lys Asp Glu Pro Lys Lys Pro Leu Thr Ile
 275 280 285

40 TAC GAC ATT ACT GCA AAA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC 912
 Tyr Asp Ile Thr Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala
 290 295 300

45 AAG GTC AAT CCT GAT TTA GCG AAA AAC CTT GCC GGT AAT GAG CGT TTG 960
 Lys Val Asn Pro Asp Leu Ala Lys Asn Leu Ala Gly Asn Glu Arg Leu
 305 310 315 320

50 TTT TTC CAT GCC GAT GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC 1008
 Phe Phe His Ala Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly
 325 330 335

	GAT AAC GGA GAA GAG CTT GCC GGA CGG TTT ATC AGC AAC GAC AAC AGC	1056
	Asp Asn Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser	
	340 345 350	
5	GTA TTC GGC GTA TTC GCA GGC AAA AAA ACA GAG ACA GCA AAC GCA GCA	1104
	Val Phe Gly Val Phe Ala Gly Lys Lys Thr Glu Thr Ala Asn Ala Ala	
	355 360 365	
10	GAT ACA AAA CCT GCC CTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT	1152
	Asp Thr Lys Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp	
	370 375 380	
15	TCT CTA AAA ATT TCC GTT GAC GAG GCG ACT GAT GGC CAT GCC CGT AAG	1200
	Ser Leu Lys Ile Ser Val Asp Glu Ala Thr Asp Gly His Ala Arg Lys	
	385 390 395 400	
20	TTT GCC ATT TCC TCT ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT	1248
	Phe Ala Ile Ser Ser Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu	
	405 410 415	
	GTC GAA GGG CGT GAA ATT CCT TTG GTA AAC GAA GAA CAA ATC ATC AAG	1296
	Val Glu Gly Arg Glu Ile Pro Leu Val Asn Glu Glu Gln Ile Ile Lys	
	420 425 430	
25	CTT GCC GAC GGC AGG AAA ATG ACC GTC CGT GCT TGT TGC GAC TTT TTG	1344
	Leu Ala Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu	
	435 440 445	
30	ACC TAT GTG AAA CTC GGA CGG ATA AAA ACC GAT CGC CCG GCA AGT AAA	1392
	Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys	
	450 455 460	
35	CCA AAG GCG GAA GAT AAA GGG GAG GAT GAA GAG GGT GCA GGC GTT GAT	1440
	Pro Lys Ala Glu Asp Lys Gly Glu Asp Glu Glu Gly Ala Gly Val Asp	
	465 470 475 480	
40	AAC GAC GAA GAA AGC GAA GAC GAA GCC GTA GAA GAC GAA GGC GGC GAA	1488
	Asn Asp Glu Glu Ser Glu Asp Glu Ala Val Glu Asp Glu Gly Gly Glu	
	485 490 495	

29

GAA GAC GAA ACT TCC GAA GAG GAT AAT GGC GAA GAC GAA GAA GCA ACC 1536
 Glu Asp Glu Thr Ser Glu Glu Asp Asn Gly Glu Asp Glu Glu Ala Thr
 500 505 510

5 GCC GAA GAA GAA ACC GAA GAA GTT GAT GAA GCC GAA GAG GAG GAA GTT 1584
 Ala Glu Glu Glu Thr Glu Glu Val Asp Glu Ala Glu Glu Glu Val
 515 520 525

GAA GAA CCC GAA GAA AAA TCG CCG GCA GAA GGC AAC GGC GGT TCA GGC 1632
 10 Glu Glu Pro Glu Glu Lys Ser Pro Ala Glu Gly Asn Gly Ser Gly
 530 535 540

AGC ATC CTG CCT GCC CTA GAA GCC TCT AAA GGC AGG GAC ATC GAC CTT 1680
 Ser Ile Leu Pro Ala Leu Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu
 15 545 550 555 560

TTC CTG AAA GGT ATC CGC ACG GCA GAA ACG GAT ATT CCG CAA AGC GGA 1728
 Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asp Ile Pro Gln Ser Gly
 565 570 575

20 ACG GCG CAT TAT ACC GGC ACT TGG GAA GCG CGT ATC GGC AAA CCC ATT 1776
 Thr Ala His Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro Ile
 580 585 590

CAA TGG GAC AAT CAG GCG GAT GAA AAA GCG GCA AAA GCA GAA TTT ACC 1824
 Gln Trp Asp Asn Gln Ala Asp Glu Lys Ala Ala Lys Ala Glu Phe Thr
 25 595 600 605

GTT GAT TTC GAC AAG AAA TCG ATT TCC GGA AAG CTG ACG GAG CAA AAC 1872
 Val Asp Phe Asp Lys Lys Ser Ile Ser Gly Lys Leu Thr Glu Gln Asn
 30 610 615 620

GGC GTA GAA CCT GCT TTC CAT ATT GAA GAC GGC AAG ATT GAT GGC AAC 1920
 Gly Val Glu Pro Ala Phe His Ile Glu Asp Gly Lys Ile Asp Gly Asn
 35 625 630 635 640

GGT TTC CAC GCG ACA GCG CGC ACT CGG GAG AGC GGC ATC AAT CTT TCG 1968
 Gly Phe His Ala Thr Ala Arg Thr Arg Glu Ser Gly Ile Asn Leu Ser
 40 645 650 655

GGA AAT GGT TCG ACC GAC CCC AAA ACA TTC CAA GCT AGT AAT CTT CGT 2016
 Gly Asn Gly Ser Thr Asp Pro Lys Thr Phe Gln Ala Ser Asn Leu Arg
 660 665 670

30

GTA GAA GGA GGA TTT TAC GGC CCG CAG GCG GCG GAA TTG GGC GGT ACT 2064
 Val Glu Gly Gly Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Thr
 675 680 685

5

ATT TTC AAT AAT GAT GGG AAA TCT CTT AGT ATA ACT GAA AAT ATT GAA 2112
 Ile Phe Asn Asn Asp Gly Lys Ser Leu Ser Ile Thr Glu Asn Ile Glu
 690 695 700

10 AAT GAA GCT GAA GCT GAA GTT GAA GCT GAA GCT GAA GCT GAA GTT GAA 2160
Asn Glu Ala Glu Ala Glu Val Glu Val Glu Ala Glu Ala Glu Val Glu
705 710 715 720

15 GTT GAA GCT GAT GTT GGC AAA CAG TTA GAA CCT GAT GAA GTT AAA CAC 2208
Val Glu Ala Asp Val Gly Lys Gln Leu Glu Pro Asp Glu Val Lys His
725 730 735

AAA TTC GGC GTG GTA TTC GGT GCG AAG AAA GAT ATG CAG GAG GTG GAA 2256
 Lys Phe Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val Glu
 20 740 745 750

AAA TGA **2262**
Lys

25

(2) INFORMATION FOR SEO ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 753 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal
 (vi) ORIGINAL SOURCE:

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu

31

Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
20 25 30

Thr Pro Thr Ala Pro Thr Leu Ser Asp Ser Lys Ser Ser Asn Pro Ala
35 40 45

5 Asp Lys Pro Ala Pro Ala Glu Pro Ser Val Glu Ile Thr Pro
50 55 60

Val Lys Arg Pro Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn
65 70 75 80

Ile Ala Thr Phe Asp Lys Asn Gly Asn Glu Ile Pro Asn Ser Lys Gln
10 85 90 95

Ala Glu Glu Tyr Leu Pro Leu Lys Glu Lys Asp Ile Leu Phe Leu Asp
100 105 110

Gly Thr Pro Lys Glu Gln Ala Asp Lys Leu Lys Lys Glu Ile Asn Gly
115 120 125

15 Arg His Pro Asn Ala Pro Ile Tyr Thr Ser Asp Leu Lys Asp Asp Ala
130 135 140

Tyr Gln Tyr Lys Tyr Val Arg Ala Gly Tyr Val Tyr Thr Arg Tyr Gly
145 150 155 160

Thr Asp Glu Ile Glu Gln Asn Ser Gly Gly Lys Arg Val Thr His Arg
20 165 170 175

Leu Gly Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln
180 185 190

Ser Leu Pro Ser Ala Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr
195 200 205

25 Met Thr Asp Ala Lys Arg His Arg Ala Gly Gln Ala Val Gly Ile Asp
210 215 220

Asn Leu Gly Tyr Ile Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser
225 230 235 240

Tyr Ala Ala Lys Asp Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr
30 245 250 255

Thr Val Asp Phe Asp Asn Lys Thr Met Asn Gly Lys Leu Ile Lys Asn
260 265 270

Gln Tyr Val Arg Asn Lys Asp Glu Pro Lys Lys Pro Leu Thr Ile
275 280 285

35 Tyr Asp Ile Thr Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala
290 295 300

Lys Val Asn Pro Asp Leu Ala Lys Asn Leu Ala Gly Asn Glu Arg Leu
305 310 315 320

Phe Phe His Ala Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly
40 325 330 335

Asp Asn Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser
340 345 350

32

Val Phe Gly Val Phe Ala Gly Lys Lys Thr Glu Thr Ala Asn Ala Ala
355 360 365
Asp Thr Lys Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp
370 375 380
5 Ser Leu Lys Ile Ser Val Asp Glu Ala Thr Asp Gly His Ala Arg Lys
385 390 395 400
Phe Ala Ile Ser Ser Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu
405 410 415
Val Glu Gly Arg Glu Ile Pro Leu Val Asn Glu Glu Gln Ile Ile Lys
10 420 425 430
Leu Ala Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu
435 440 445
Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys
450 455 460
15 Pro Lys Ala Glu Asp Lys Gly Glu Asp Glu Glu Gly Ala Gly Val Asp
465 470 475 480
Asn Asp Glu Glu Ser Glu Asp Glu Ala Val Glu Asp Glu Gly Glu
485 490 495
Glu Asp Glu Thr Ser Glu Glu Asp Asn Gly Glu Asp Glu Glu Ala Thr
20 500 505 510
Ala Glu Glu Glu Thr Glu Glu Val Asp Glu Ala Glu Glu Glu Val
515 520 525
Glu Glu Pro Glu Glu Lys Ser Pro Ala Glu Gly Asn Gly Gly Ser Gly
530 535 540
25 Ser Ile Leu Pro Ala Leu Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu
545 550 555 560
Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asp Ile Pro Gln Ser Gly
565 570 575
Thr Ala His Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro Ile
30 580 585 590
Gln Trp Asp Asn Gln Ala Asp Glu Lys Ala Ala Lys Ala Glu Phe Thr
595 600 605
Val Asp Phe Asp Lys Lys Ser Ile Ser Gly Lys Leu Thr Glu Gln Asn
610 615 620
35 Gly Val Glu Pro Ala Phe His Ile Glu Asp Gly Lys Ile Asp Gly Asn
625 630 635 640
Gly Phe His Ala Thr Ala Arg Thr Arg Glu Ser Gly Ile Asn Leu Ser
645 650 655
Gly Asn Gly Ser Thr Asp Pro Lys Thr Phe Gln Ala Ser Asn Leu Arg
40 660 665 670
Val Glu Gly Gly Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Thr
675 680 685

33

Ile Phe Asn Asn Asp Gly Lys Ser Leu Ser Ile Thr Glu Asn Ile Glu
 690 695 700
 Asn Glu Ala Glu Ala Glu Val Glu Val Glu Ala Glu Ala Glu Val Glu
 705 710 715 720
 5 Val Glu Ala Asp Val Gly Lys Gln Leu Glu Pro Asp Glu Val Lys His
 725 730 735
 Lys Phe Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val Glu
 740 745 750

Lys

10

15

(2) INFORMATION FOR SEQ ID NO:9:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(B) STRAIN: Neisseria meningitidis strain 881607

30

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2121

(D) OTHER INFORMATION:

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG
 Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 35 1. 5 10 15

48

GCA TCT TGC ATC GGC GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA
 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
 20 25 30

96

40

ACG CCG ACC GCG TAC CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT
 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
 35 40 45

144

	TCG CCT CCT GCC GGG TCT TCG GTA GAA ACC ACG CCG GTC AAC CGA CCC	192	
	Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Arg Pro		
50	55	60	
5			
	GCC GTT GGT GCG GCA ATG CGG CTG TTG AGA CGG AAT ATT GCA ACT TCT	240	
	Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Ile Ala Thr Ser		
65	70	75	
		80	
10			
	GAT AAG GAT GGC AAT GAT TTT CCA AAT AGC AAA CAA GCA GAA GAA AAG	288	
	Asp Lys Asp Asp Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu Glu Lys		
	85	90	95
15			
	CTG TCG TTT AAA GAG GAA GAT ATC CTG TTT TTA TAC GGT TCC AAA AAA	336	
	Leu Ser Phe Lys Glu Glu Asp Ile Leu Phe Leu Tyr Gly Ser Lys Lys		
	100	105	110
20			
	GAT CAA CGT CAG CAG CTT AAA GAT AAA ATT CGT CAA CCA AAT CCT ACG	384	
	Asp Gln Arg Gln Gln Leu Lys Asp Lys Ile Arg Gln Pro Asn Pro Thr		
	115	120	125
25			
	GCA AGC ATT ACC ACA TCG GAA AAG AAA AAT AAA AAA TAT GAT TAT AAA	432	
	Ala Ser Ile Thr Thr Ser Glu Lys Lys Asn Lys Lys Tyr Asp Tyr Lys		
	130	135	140
	TTT GTA GAT GCA GGT TAT GTA TAT ACT AAA GAC GGA AAA GAT GAA ATT	480	
	Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asp Gly Lys Asp Glu Ile		
	145	150	155
		160	
30			
	GAG TGG ACT TCA AAT TAC AAG CAG TCT ACC AAC CGG TTT GGT TAT GAC	528	
	Glu Trp Thr Ser Asn Tyr Lys Gln Ser Thr Asn Arg Phe Gly Tyr Asp		
	165	170	175
35			
	GGT TTT GTA TAT TAT TCC GGA GAA CAT CCT TCG CAA TCT TTA CCG AGC	576	
	Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu Pro Ser		
	180	185	190
40			
	GCG GGA ACG GTG AAA TAT TCC GGC AAC TGG CAA TAT ATG ACC GAT GCC	624	
	Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala		
	195	200	205

	35		
ATA CGT CAT CGA ACA GGA AAA GCA GGA GAT CCT AGC GAA GAT TTG GGT			672
Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp Leu Gly			
210	215	220	
 5			
TAT ATC GTT TAT TAC GGT CAA AAT GTC GGA GCA ACT TCT TAT GCT GCG			720
Tyr Ile Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr Ala Ala			
225	230	235	240
 10			
ACT GCC GAC GAC CGG GAG GGA AAA CAT CCT GCC GAA TAT ACG GTT AAT			768
Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr Val Asn			
245	250	255	
 15			
TTC GAC CAA AAA ACT CTG AAT GGC AAG CTG ATT AAA AAT CAG TAT GTG			816
Phe Asp Gln Lys Thr Leu Asn Gly Lys Leu Ile Lys Asn Gln Tyr Val			
260	265	270	
 20			
CAA AAG AGA GAT GAT CCT AAA AAA CCA CTG ACC ATT TAC GAC ATT ACT			864
Gln Lys Arg Asp Asp Pro Lys Lys Pro Leu Thr Ile Tyr Asp Ile Thr			
275	280	285	
 25			
GCA AAA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC AAA GTT AAC ACA			912
Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Thr			
290	295	300	
 30			
GAG GTG AAG ACG AAT CAC GCT GAT AAA GAA TAT TTG TTT TTC CAT ACC			960
Glu Val Lys Thr Asn His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr			
305	310	315	320
 35			
GAT GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC GAT AAG GGG GAA			1008
Asp Ala Asp Gln Arg Leu Glu Gly Phe Phe Gly Asp Lys Gly Glu			
325	330	335	
 40			
GAG CTT GCC GGA CGG TTT ATC AGC AAC GAC AAC AGC GTA TTC GGC GTG			1056
Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val			
340	345	350	
 355			
TTC GCA GGC AAA CAA AAA ACA GAG ACA GCA AAC GCA TCA GAT ACA AAT			1104
Phe Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn			
355	360	365	
 370			
CCT GCC CTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT TCT CTA AAA			1152
Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys			
370	375	380	

	ATT TCC GTT GAC GAG GCA AGT GGT GAA AAT CCC CGA CCG TTT GAG GTT Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Glu Val 385	390	395	400	1200
5	TCC ACT ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT GTC GAA GGG Ser Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly 405	410	415		1248
10	CGT GAA ATT CCT TTG GTA AAC AAA GAA CAA ACC ATC GAT CTT GCC GAC Arg Glu Ile Pro Leu Val Asn Lys Glu Gln Thr Ile Asp Leu Ala Asp 420	425	430		1296
15	GGC AGG AAA ATG ACC GTC CGT GCT TGT TGC GAC TTT TTG ACC TAT GTG Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val 435	440	445		1344
20	AAA CTC GGA CGG ATA AAA ACC GAA CGC CCC GCC GTC CAA CCG AAG GCG Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Val Gln Pro Lys Ala 450	455	460		1392
25	CAG GAT GAA GAG GGG GAC GAA GAG GGT GTA GGC GTT GAT AAC GGT AAA Gln Asp Glu Glu Gly Asp Glu Glu Gly Val Gly Val Asp Asn Gly Lys 465	470	475	480	1440
30	GAA AGC GAA GAC GAA ATC GGC GAT GAA GAA AGC ACC GGA GAC GAA GTC Glu Ser Glu Asp Glu Ile Gly Asp Glu Ser Thr Gly Asp Glu Val 485	490	495		1488
35	GTA GAA GAT GAA GAC GAA GAT GAA GAC GAA GAA GAA ATC GAA GAA GAA Val Glu Asp Glu Asp Glu Asp Glu Asp Glu Glu Glu Ile Glu Glu Glu 500	505	510		1536
40	CCT GAA GAA GAA GCT GAA GAG GAA GAA CCC GAA GAA GAA TTG CCG GCA Pro Glu Glu Glu Ala Glu Glu Glu Pro Glu Glu Glu Leu Pro Ala 515	520	525		1584
	GAA GAA GGC AAC GGC GGT TCA GGC AGC ATC CTG CCC ACT CCG GAA GCC Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala 530	535	540		1632

	37		
TCT AAA GGC AGG GAC ATC GAC CTT TTC CTG AAA GGT ATC CGC ACG GCG			1680
Ser Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala			
545	550	555	560
 5 GAA GCC GAC ATT CCA AAA AAC GGA ACG GCG CAT TAT ACC GGC ACT TGG			1728
Glu Ala Asp Ile Pro Lys Asn Gly Thr Ala His Tyr Thr Gly Thr Trp			
565	570		575
 10 GAA GCG CGT ATC GGC GTA TCG GAT AGT GGT ACG TCC ATT CAA AAG GAT			1776
Glu Ala Arg Ile Gly Val Ser Asp Ser Gly Thr Ser Ile Gln Lys Asp			
580	585	590	
 15 AGC TAT GCG AAT CAA GGG GCA AAA GCA GAA TTT ACC GTT GAT TTC GAA			1824
Ser Tyr Ala Asn Gln Gly Ala Lys Ala Glu Phe Thr Val Asp Phe Glu			
595	600	605	
 20 GCG AAG ACG GTG TCC GGA ATG CTG ACA GAA AAA AAT GAT ACA ACC CCC			1872
Ala Lys Thr Val Ser Gly Met Leu Thr Glu Lys Asn Asp Thr Thr Pro			
610	615	620	
 25 GCT TTT TAT ATT GAA AAA GGT GTG ATT GAC GGT AAC GGT TTC CAC GCT			1920
Ala Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala			
625	630	635	640
 30 TTG GCG CAT ACT CGG GAG AAC GGT ATT GAC CTT TCT GGG CAG GGT TCG			1968
Leu Ala His Thr Arg Glu Asn Gly Ile Asp Leu Ser Gly Gln Gly Ser			
645	650	655	
 35 ACT AAC CCG AAG AAC TTC AAA GCC GAC AAT CTT CTT GTA ACA GGC GGC			2016
Thr Asn Pro Lys Asn Phe Lys Ala Asp Asn Leu Leu Val Thr Gly Gly			
660	665	670	
 40 TTT TAT GGC CCG CAG GCG GCA GAA TTG GGC GGT AAT ATT ATC GAC AGC			2064
Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser			
675	680	685	
 45 GAC CGG AAA TTC GGT GCG GTA TTT GGG GCG AAA AAA GAT GAC AAG GAG			2112
Asp Arg Lys Phe Gly Ala Val Phe Gly Ala Lys Lys Asp Asp Lys Glu			
690	695	700	
 50 GCA ACA CGA TGA			2124
Ala Thr Arg			
705			

(2) INFORMATION FOR SEQ ID NO:10:

39

Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp Leu Gly
210 215 220
Tyr Ile Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr Ala Ala
225 230 235 240
5 Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr Val Asn
245 250 255
Phe Asp Gln Lys Thr Leu Asn Gly Lys Leu Ile Lys Asn Gln Tyr Val
260 265 270
Gln Lys Arg Asp Asp Pro Lys Lys Pro Leu Thr Ile Tyr Asp Ile Thr
10 275 280 285
Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Thr
290 295 300
Glu Val Lys Thr Asn His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr
305 310 315 320
15 Asp Ala Asp Gln Arg Leu Glu Gly Phe Phe Gly Asp Lys Gly Glu
325 330 335
Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val
340 345 350
Phe Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn
20 355 360 365
Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys
370 375 380
Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Glu Val
385 390 395 400
25 Ser Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly
405 410 415
Arg Glu Ile Pro Leu Val Asn Lys Glu Gln Thr Ile Asp Leu Ala Asp
420 425 430
Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val
30 435 440 445
Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Val Gln Pro Lys Ala
450 455 460
Gln Asp Glu Glu Gly Asp Glu Glu Gly Val Gly Val Asp Asn Gly Lys
465 470 475 480
35 Glu Ser Glu Asp Glu Ile Gly Asp Glu Glu Ser Thr Gly Asp Glu Val
485 490 495
Val Glu Asp Glu Asp Glu Asp Glu Asp Glu Glu Glu Ile Glu Glu Glu
500 505 510
Pro Glu Glu Glu Ala Glu Glu Glu Pro Glu Glu Glu Leu Pro Ala
40 515 520 525
Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala
530 535 540

40

Ser Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala
545 550 555 560
Glu Ala Asp Ile Pro Lys Asn Gly Thr Ala His Tyr Thr Gly Thr Trp
565 570 575
5 Glu Ala Arg Ile Gly Val Ser Asp Ser Gly Thr Ser Ile Gln Lys Asp
580 585 590
Ser Tyr Ala Asn Gln Gly Ala Lys Ala Glu Phe Thr Val Asp Phe Glu
595 600 605
Ala Lys Thr Val Ser Gly Met Leu Thr Glu Lys Asn Asp Thr Thr Pro
10 610 615 620
Ala Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala
625 630 635 640
Leu Ala His Thr Arg Glu Asn Gly Ile Asp Leu Ser Gly Gln Gly Ser
645 650 655
15 Thr Asn Pro Lys Asn Phe Lys Ala Asp Asn Leu Leu Val Thr Gly Gly
660 665 670
Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser
675 680 685
Asp Arg Lys Phe Gly Ala Val Phe Gly Ala Lys Lys Asp Asp Lys Glu
20 690 695 700
Ala Thr Arg
705